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RAW SEQUENCE LISTING

DATE: 03/12/2002

PATENT APPLICATION: US/09/873,829

TIME: 09:54:51

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\1873829.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Choi, Yongwon
                             Wong, Brian
      б
      7
                             Josien, Regis
      8
                             Steinman, Ralph
            (ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
     10
     11
                                       INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
SAME, AND
     1.2
                                      METHODS OF USE THEREOF
     14
           (iii) NUMBER OF SEQUENCES: 18
     16
            (iv) CORRESPONDENCE ADDRESS:
     17
                  (A) ADDRESSEE: Klauber & Jackson
     18
                   (B) SIREET: 411 Hackensack Avenue, 4th Floor
     19
                  (C) CITY: Hackensack
     20
                  (D) STATE: New Jersey
     21
                  (E) COUNTRY: USA
     22
                  (F) ZIP: 07601
     24
             (V) COMPUTER READABLE FORM:
     25
                  (A) MEDIUM TYPE: Floppy disk
     26
                  (B) COMPUTER: IBM PC compatible
     27
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     28
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     30
            (vi) CUERENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/873,829
C--> 31
C--> 32
                  (B) FILING DATE: 04-Jun-2001
     3.3
                  (C) CLASSIFICATION:
     35
           (vii) PRIOR APPLICATION DATA:
                  (A) APPLICATION NUMBER: 09/210,115
     36
     37
                  (B) FILING DATE:
          (viii) ATTORNEY/AGENT INFORMATION:
     4()
     4.1
                  (A) NAME: Jackson Esq., David A.
     4.2
                  (B) REGISTRATION NUMBER: 26,742
                  (C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N
     43
     45
            (ix) TELECOMMUNICATION INFORMATION:
     46
                  (A) TELEPHONE: 201-487-5800
     47
                  (B) TELEFAX: 201-343-1684
     48
                  (C) TELEX: 133521
     51 (2) INFORMATION FOR SEQ ID NO: 1:
     53
             (i) SEQUENCE CHARACTERISTICS:
     54
                  (A) LENGTH: 1823 base pairs
     55
                  (B) TYPE: nucleic acid
     56
                  (C) STRANDEDNESS: double
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(D) TOPOLOGY: linear

57

PATE: 03/12/2002

Input Set : N:\Crf3\RULE60\09873829.raw Output Set: N:\CRF3\03122002\1873829.raw

59 (ii) MOLECULE TYPE DDNA	
6] (iii) HYPOTHETICAL: NO	
63 (vi) ORIGINAL SOURCE:	
64 (A) ORGANISM: Homo sapiens	
66 (ix) FEATURE:	
6' (A) NAME/KEY. CDS	
68 (B) LOCATION: 1738	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
73 CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT	48
74 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr	
75 1 5 10 15	
77 AGA ATI TIG AGA CIC CAI GAA AAI GCA GAI TII CAA GAC ACA ACI CIG	96
78 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu	
79 20 25 30	
81 GAG AGI CAA GAI ACA AAA ITA ATA CCI GAI TCA IGI AGG AGA ATI AAA	144
82 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys	
83 35 40 45	
85 CAG GCC TII CAA GGA GCI GTG CAA AAG GAA TIA CAA CAI ATC GTT GGA	192
86 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly	
87 50 55 60	
8+ TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA	240
90 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu	
91. 65 70 75 80	
93 GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC	288
94 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu	
95 85 90 95	
97 ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG	336
98 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu	
99 100 105 110	201
101 TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT	384
102 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr	
103 115 120 125	422
105 TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAI TAC CTG	432
106 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu	
107 130 135 140	480
109 TAT GCC AAC AIT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT	400
110 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala 111 145 150 150 155	
111 145 150 150 155 160 113 ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA	528
114 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys	220
114 Thi Gid Tyl Led Gill Led Met val Tyl val Thi Lys Thi Set Tie Lys 115 165 170 175	
117 ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG	576
118 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp	3,0
119 180 185 190	
121 ICA GGG AAT TCT GAA TTC CAT TTT TAT ICC ATA AAC GTT GGT GGA TTT	624
122 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe	521
123 195 200 205	
125 TIT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC	672
126 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro	

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Input Set : N:\Crf3\RULE60\09873829.raw
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127		210					215					220					
	TCC		CIG	GAT	CCG	GAT			GCA	ACA	TAC		GGG	GCT	TTT	AAA	720
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	225	-,-				230					235		:			240	
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135		,			245												
	IGGA	AIGI	TTG	GAAA		гт т	TAAA	ACAA(G CC	AAGAZ	AAGA	TGI	A LA L	AGG	TGTG	rgagad	828
																GTAGAG	
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145	AIGA	AGAA.	ACT	GCAT	g Tigigi	GC T	A TIGG	GAGGG	G GT	IGGI	CCCT	GGT	CATG	rge -	CCCT:	regeag	1068
147	CIGA	AAGT	GGA	GAGG	GIGT	CA T	CTAG	CGCAA	A TT	GAAG	GATC	ATC:	rgaa(GGG	GCAAA	ATTOTT	1128
149	TTGA	AATT	GTT	ACAT	CATG	CT G	GAAC	CIGCA	A AA	AAAT	ACTT	гтг	СТАА	TGA	GGAGA	AGAAAA	1188
15.1	TATA	ATGT	TTA	TITA	TATA	AT A	ICTA	AAGT:	T AT	ATTT	CAGA	IGTA	AATG	TTT	TCTT	IGCAAA	1248
153	GTA:	TGT	AAA	TTAT	ATTT	GT G	CTATA	AGTA:	г тт	GATT	CAAA	ATA:	ГТТА	AAA .	ATGT	CITGCI	1308
155	GTT	GACA	TAT	TIAA	IGIT	IT A	AA [G]	TACA	G AC	ATAT	AATT	CTG	GTGC	ACT	TIGIA	AAATTO	1368
157	CCTO	GGGG.	AAA	ACIT	GCAG	CT A	Α ΙΞΙΞΑΙ	3GGGA	A AA	TAAA	GTTG	TTT	CCTA	ATA	TCAAA	ATGCAG	1428
159	TATA	TTTA	CTT	CGIT	CTTT	ГТ А	AGTT	AATA	G AT	ГТТТ	rcag	ACT:	rgrez	AAG	CCTG	rgcaaa	1488
161	AAAA	ATTA	AAA	TGGA	rgcc:	IT G	AATAA	ATAA	G CA	GGAT:	STTG	GCCA	ACCA	GGT (GCCT:	ETCAAA	1548
163	TTTA	AGAA	ACT	AATT	GACT	ET A	GAAA	GCTGA	A CA	FIGC	CAAA	AAG	GATA	CAT .	AATG	GGCCAC	1608
165	IGAA	AATC	IGT	CAAGA	AGTA	GT T	ATATA	AATTO	G TT	GAACA	AGGT	GTT	TTTC	CAC .	AAGT(GCCGCA	1668
167	AAT.	rgta(CCT	LLLL	TTGT	T T	ITTC	AAAA	r AG	AAAA	GTTA	TTA	GTGG:	TTT .	ATCAC	GCAAAA	
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181		•	() MO	D) TO	LE T	PE:	prot	tein	י בי	TD NV) · ')						
183		(xi	() MO) SE	D) TO LECUI QUENO	LE T	PE: ESCE.	prot PTI	tein DN: S					Иiс	Cyc	Tlo	Tur	
183 185	Gln	(xi	() MO) SE	D) TO LECUI QUENO	LE TI CE DI Asn	PE: ESCE.	prot PTI	tein DN: S		Asp			His	Cys	Ile 15	Tyr	
183 185 186	Gln 1	(xi Met	() MO) SE Asp	D) TO LECUI QUENO Pro	LE TI CE DI Asn 5	(PE: ESCE. Arg	prot IPTIC Ile	tein ON: S Ser	Glu	Asp 10	Gly	Thr			15		
183 185 186 188	Gln 1	(xi Met	() MO) SE Asp	D) TO LECUI QUENO Pro Arg	LE TI CE DI Asn 5	(PE: ESCE. Arg	prot IPTIC Ile	tein ON: S Ser	Glu Ala	Asp 10	Gly	Thr		Thr			
183 185 186 188 189	Gln 1 Arg	(xi Met Ile	() MO) SE Asp Leu	D) TO LECUI QUENO Pro Arg 20	DE TY DE DI Asn 5 Leu	(PE: ESCE Arg His	prot IPTIC Ile Glu	tein ON: S Ser Asn	Glu Ala 25	Asp 10 Asp	Gly Phe	Thr Gln	Asp	Thr	15 Thr	Leu	
183 185 186 188 189	Gln 1 Arg	(xi Met Ile	()) MO) SE Asp Leu Gln	D) TO LECUI QUENO Pro Arg 20	DE TY DE DI Asn 5 Leu	(PE: ESCE Arg His	prot IPTIC Ile Glu	tein ON: S Ser Asn Ile	Glu Ala 25	Asp 10 Asp	Gly Phe	Thr Gln	Asp Arg	Thr	15	Leu	
183 185 186 188 189 191	Gln 1 Arg Glu	(xi Met Ile Ser	() MO) SE Asp Leu Gln 35	D) TO LECUI QUENO Pro Arg 20 Asp	LE TY DE DI Asn 5 Leu Thr	(PE: ESCE Arg His Lys	prot IPTIC Ile Glu Leu	tein ON: S Ser Asn Ile 40	Glu Ala 25 Pro	Asp 10 Asp Asp	Gly Phe Ser	Thr Gln Cys	Asp Arg 45	Thr 30 Arg	15 Thr Ile	Leu Lys	
183 185 186 188 189 191 192	Gln 1 Arg Glu	(xi Met Ile Ser	() MO) SEA	D) TO LECUI QUENO Pro Arg 20 Asp	LE TY Asn 5 Leu Thr	(PE: ESCE Arg His Lys	prot IPTIC Ile Glu Leu Val	tein ON: S Ser Asn Ile 40 Gln	Glu Ala 25 Pro	Asp 10 Asp Asp	Gly Phe Ser Leu	Thr Gln Cys Gln	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys	
183 185 186 188 189 191 192 194 195	Gln 1 Arg Glu Gln	(xi Met Ile Ser Ala 50	() MO) SE Asp Leu Gln 35 Phe	D) TO LECUI QUENG Pro Arg 20 Asp	LE TY Asn 5 Leu Thr	(PE: ESCE Arg His Lys	prot IPTIC Ile Glu Leu Val	tein ON: S Ser Asn Ile 40 Gln	Glu Ala 25 Pro Lys	Asp 10 Asp Asp Glu	Gly Phe Ser Leu	Thr Gln Cys Gln 60	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys Gly	
183 185 186 188 189 191 192 194 195	Gln 1 Arg Glu Gln	(xi Met Ile Ser Ala 50	() MO) SE Asp Leu Gln 35 Phe	D) TO LECUI QUENG Pro Arg 20 Asp	LE TY Asn 5 Leu Thr	(PE: ESCE Arg His Lys	prot IPTIC Ile Glu Leu Val	tein ON: S Ser Asn Ile 40 Gln	Glu Ala 25 Pro Lys	Asp 10 Asp Asp Glu	Gly Phe Ser Leu	Thr Gln Cys Gln 60	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys Gly	
183 185 186 188 189 191 192 194 195 197	Gln 1 Arg Glu Gln Ser 65	(xi Met Ile Ser Ala 50 Gln	() MO) SEASP Leu Gln 35 Phe	D) TO LECUI QUENC Pro Arg 20 Asp Gln	DE TY Asn 5 Leu Thr Gly Arg	PE: ESCE. Arg His Lys Ala Ala	prot IPTI€ Ile Glu Leu Val 55 Glu	tein ON: S Ser Asn Ile 40 Gln Lys	Glu Ala 25 Pro Lys Ala	Asp 10 Asp Asp Glu Met	Gly Phe Ser Leu Val 75	Thr Gln Cys Gln 60 Asp	Asp Arg 45 His	Thr 30 Arg Ile Ser	15 Thr Ile Val	Leu Lys Gly Leu 80	
183 185 186 188 189 191 192 194 195 197	Gln 1 Arg Glu Gln Ser 65	(xi Met Ile Ser Ala 50 Gln	() MO) SEASP Leu Gln 35 Phe	D) TO LECUI QUENC Pro Arg 20 Asp Gln	DE TY Asn 5 Leu Thr Gly Arg	PE: ESCE. Arg His Lys Ala Ala	prot IPTI€ Ile Glu Leu Val 55 Glu	tein ON: S Ser Asn Ile 40 Gln Lys	Glu Ala 25 Pro Lys Ala	Asp 10 Asp Asp Glu Met	Gly Phe Ser Leu Val 75	Thr Gln Cys Gln 60 Asp	Asp Arg 45 His	Thr 30 Arg Ile Ser	15 Thr Ile Val Irp	Leu Lys Gly Leu 80	
183 185 186 188 191 192 194 195 197 198 200 201	Gln 1 Arg Glu Gln Ser 65 Asp	(xi Met Ile Ser Ala 50 Gln Leu	() MO) SE Asp Leu Gln 35 Phe His	D) TO LECUI QUENO Pro Arg 20 Asp Gln Ile	CE TY Asn 5 Leu Thr Gly Arg Arg 85	APE: Arg His Lys Ala Ala 70 Ser	prof IPTIC Ile Glu Leu Val 55 Glu Lys	tein ON: S Ser Asn Ile 40 Gln Lys Leu	Glu Ala 25 Pro Lys Ala Glu	Asp 10 Asp Asp Glu Met Ala 90	Gly Phe Ser Leu Val 75 Gln	Thr Gln Cys Gln 60 Asp	Asp Arg 45 His Gly Phe	Thr 30 Arg Ile Ser Ala	15 Thr Ile Val Trp	Leu Lys Gly Leu 80 Leu	
183 185 186 188 191 192 194 195 197 198 200 201 203 204	Gln 1 Arg Glu Gln Ser 65 Asp	(xi Met Ile Ser Ala 50 Gln Leu Ile	() MO) SE Asp Leu Gln 35 Phe His Ala	D) TO LECUI QUENO Pro Arg 20 Asp Gln Ile Lys Ala 100	LE TY Asn 5 Leu Thr Gly Arg Arg 85 Thr	APE: ESCE. Arg His Lys Ala Ala 70 Ser Asp	prot IPTIC Ile Glu Leu Val 55 Glu Lys Ile	Ser Asn Ile 40 Gln Lys Leu Pro	Glu Ala 25 Pro Lys Ala Glu Ser 105	Asp 10 Asp Asp Glu Met Ala 90 Gly	Gly Phe Ser Leu Val 75 Gln Ser	Thr Gln Cys Gln 60 Asp Pro His	Asp Arg 45 His Gly Phe Lys	Thr 30 Arg Ile Ser Ala Val 110	15 Thr Ile Val Trp His 95 Ser	Leu Lys Gly Leu 80 Leu	
183 185 186 188 189 191 192 194 195 197 198 200 201 203 204 206	Gln 1 Arg Glu Gln Ser 65 Asp	(xi Met Ile Ser Ala 50 Gln Leu Ile	() MO) SE Asp Leu Gln 35 Phe His Ala Asn Trp	D) TO LECUI QUENO Pro Arg 20 Asp Gln Ile Lys Ala 100	LE TY Asn 5 Leu Thr Gly Arg Arg 85 Thr	APE: ESCE. Arg His Lys Ala Ala 70 Ser Asp	prot IPTIC Ile Glu Leu Val 55 Glu Lys Ile	tein ON: S Ser Asn Ile 40 Gln Lys Leu Pro Gly	Glu Ala 25 Pro Lys Ala Glu Ser 105	Asp 10 Asp Asp Glu Met Ala 90 Gly	Gly Phe Ser Leu Val 75 Gln Ser	Thr Gln Cys Gln 60 Asp Pro His	Asp Arg 45 His Gly Phe Lys	Thr 30 Arg Ile Ser Ala Val 110	15 Thr Ile Val Irp His 95	Leu Lys Gly Leu 80 Leu	
183 185 186 188 189 191 192 194 195 197 200 201 203 204 206 207	Gln 1 Arg Glu Gln Ser 65 Asp Thr	(xi Met Ile Ser Ala 50 Gln Leu Ile Ser	Gln 35 Phe His Ala Asn Trp 115	D) TO LECUI QUENO Pro Arg 20 Asp Gln Ile Lys Ala 100 Tyr	LE TY Asn 5 Leu Thr Gly Arg Arg Arg His	APE: ESCE Arg His Lys Ala 70 Ser Asp	prot IPTIC Ile Glu Leu Val 55 Glu Lys Ile Arg	Leu Pro Gly 120	Glu Ala 25 Pro Lys Ala Glu Ser 105 Trp	Asp 10 Asp Asp Glu Met Ala 90 Gly Gly	Gly Phe Ser Leu Val 75 Gln Ser Lys	Thr Gln Cys Gln 60 Asp Pro His	Asp 45 His Gly Phe Lys Ser 125	Thr 30 Arg Ile Ser Ala Val 110 Asn	15 Thr Ile Val Trp His 95 Ser	Leu Lys Gly Leu 80 Leu Leu Leu	

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Output Set: N:\CRF3\03122002\1873829.raw

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213	2 Tyr		ASII	rre			Arg	ніѕ	HIS	GIU		Ser	GIY	ASP	Leu		
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21)		D	Q	a	165	T 1			T	170	21	Q	T1	•	175 T	T	
	d Ile	Pro	ser		HlS	inr	Leu	мет		GIŸ	Gly	Ser	lnr		Tyr	Trp	
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246						SM:	Mus	muso	culus	3							
248	3	(ix)	FEA	TURE	Ξ:			muso	culus	3							
248 248	3 . 1	(ix)	FEA (A	TURE A) NA	E: AME/K	KEY:	CDS			6							
248 248 25)	3 ≄ ∪		FEA (A	ATURE A) NA B) LO	E: AME/K DCATI	KEY:	CDS 142.	.109	92								
248 248 250 25	3 3	(xi)	FEA (A (E SEQ	ATURE A) NA B) LO QUENO	E: AME/K DCATI DE DE	KEY: ION: ESCRI	CDS 142.	109 ON: S) SEQ 1	id n o							
248 248 250 25 258	3 3 1 3 5 aac	(xi) ACGIO	FEA (A (E SEQ	ATURE A) NA B) LO QUENO GGGGA	E: AME/K DCATI DE DE AGCCA	KEY: ION: ESCRI AC TO	CDS 142. PTIC	109 DN: S	92 SEQ 1	ID n o	AACC	GGTC				CCGIGG	60
248 248 25 25 25 25	3 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	(xi) ACGIC AGTCI	FEA (A (E SEQ CCC G	TURE A) NA B) LO QUENC GGGGA TOGGO	E: AME/K DCATI DE DE AGCCA DGGTG	KEY: ION: ISCRI IC TO	CDS 142. PTIC CCAC	109 DN: S GGACC	92 SEQ 1 S TT1 S AAC	ID NO IGTGA GGGAO	AACC SAGA	GGTC ACGA	TCGC	ogg A	AGCAC	GGCGC	120
248 248 250 25 255 257 257	3 ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;;	(xi) ACGIC AGTCI	FEA (A (E SEQ CCC G	TURE A) NA B) LO QUENC GGGGA TOGGO	E: AME/K DCATI DE DE AGCCA DGGTG	KEY: ION: ISCRI IC TO	CDS 142. PTIC GCCAC GGCC AIG	109 DN: S GGACC CCGAC CGC	92 SEQ 1 TTT G AAC CGG	ID NO IGTGA GGGAC GCC	AACC SAGA AGC	GGTC ACGA CGA	TCGC GAC	CGG A	AGCAC GGC	GGCGC AAG	
248 248 250 25 255 257 257	3 ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;;	(xi) ACGIC AGTCI	FEA (A (E SEQ CCC G	TURE A) NA B) LO QUENC GGGGA TOGGO	E: AME/K DCATI DE DE AGCCA DGGTG	KEY: ION: ISCRI IC TO	CDS 142. PTIC GCCAC GGCC AIG	109 DN: S GGACC	92 SEQ 1 TTT G AAC CGG	ID NO IGIGA GGGAO GCC Ala	AACC SAGA AGC	GGTC ACGA CGA	TCGC GAC	CGG A	AGCAC GGC Gly	GGCGC AAG	120
248 249 250 25 255 257 260 -> 26 1	3 ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;; ;;	(xi) ACGIC AGICI	FEA (A (E SEQ CCC G GGC I	ATURE A) NA B) LO BUENC GGGG GGGG GGGGC GGGGC	E: AME/K DCATI DE DE AGCCA DCGCG	KEY: ION: ISCRI AC TO GG GI GC C	CDS 142. PTIC GCCAC GGCC AIG Met	109 DN: S GGACC CCGAC CGC Arg	92 SEQ 1 S TII G AAC CGG Arg	ID NO IGIGA GGGAC GCC Ala 250	AACC SAGA AGC Ser	GGTC ACGA CGA Arg	TCGC GAC Asp	EGG A TAC Tyr	AGCAC GGC Gly 255	GGGCGC AAG Lys	120 171
248 248 250 25 255 257 260 -> 261 263	3 3 5 CCC. 7 CGG. 4 CCG. 1 L	(xi) ACGIC AGTCT AACIC	FEA (A (E SEQ CCC G GCC T GCC G	ATURE A) NA B) LO QUENC GGGGA GGGGC GGGGC AGC	E: AME/K DCATI CE DE AGCCA CCGCG CCGCG	KEY: FON: ESCRI AC TO GG GI GC C	CDS 142. EPTIC GCCAC GGCC AIG Met	109 DN: S GGACC CCGAC CGC Arg	92 SEQ 1 C TII G AAC CGG Arg	ID NO IGIGA GGC GCC Ala 250 AGC	AACC GAGA AGC Ser	GGTC ACGA CGA Arg	TCGC GAC Asp GGC	CGG A TAC Tyr GTC	AGCAC GGC Gly 255 CCA	GGGCGC AAG Lys CAC	120
248 248 250 251 251 251 261 261 263	3 3 5 ccc. 7 ccc. 4 ccc. 1 1 1 1 1 1 1 1 1 1 1 1 1	(xi) ACGIC AGTCT AACIC	FEA (A (E SEQ CCC G GCC T GCC G	ATUREA) NA A) NA B) LO QUENC GGGGG GGGGC AGC Ser	E: AME/K DCATI CE DE AGCCA CCGCG CCGCG	KEY: FON: ESCRI AC TO GG GI GC C	CDS 142. EPTIC GCCAC GGCC AIG Met	109 DN: S GGACC CCGAC CGC Arg	BEQ 1 EEQ 1 E TII EGG CGG Arg	ID NO IGIGA GGC GCC Ala 250 AGC	AACC GAGA AGC Ser	GGTC ACGA CGA Arg	TCGC GAC Asp GGC	GGG A TAC Tyr GTC Val	AGCAC GGC Gly 255 CCA	GGGCGC AAG Lys CAC	120 171
248 249 250 250 251 260 -> 261 264 -> 265	3 3 5	(xi) ACGIC AGICI AACIC CTG Leu	FEA (A (E SEC GC I GCG G CGC Arg	ATUREAL) NA A) LO QUENC GGGGG GGGGC AGC Ser 260	E: AME/K DCATI DE DE AGCCA DGGTG DCGCG TCG Ser	GEY: GON: ESCRI GG GI GC C GAA Glu	CDS 142. EPTIC GCCAC GGGCO AIG Met GAG Glu	109 DN: S GGACC CCGAC CGC Arg ATG Met	BEQ DESERVED TO THE SERVED TO	ID NO IGIGA GGGAC GCC Ala 250 AGC Ser	AACC GAGA AGC Ser GGC Gly	GGTC ACGA CGA Arg CCC Pro	GAC GAC Asp GGC Gly	GGG A TAC Tyr GTC Val 270	AGCAC GGC Gly 255 CCA Pro	GGGCGC AAG Lys CAC His	120 171 219
248 248 250 25 255 257 260 260 264 -> 265 267	3 3 3 5 CCC 7 CGG. 4 CCG. 1 1 1 1 1 1 1 1 7 GAA	(xi) ACGIC AGTCT AACTC CTG Leu GGT	FÉA (A (E SEQ CCC G GGC T CCG G	ATUREAN NAME OF THE PROPERTY O	E: AME/K DCATI DE DE AGCCA CGGCG TCG Ser CAC	GEY: ION: ESCRI GC TO GG GI GAA Glu	CDS 142. PTIC GCCAC GGCC AIG Met GAG Glu	109 DN: S GGACC CCGAC CGC Arg ATG Met	BEQ DESEQUENCE OF THE COMMENT OF THE	ID NO IGIGA GGGAC Ala 250 AGC Ser	AACC GAGA AGC Ser GGC Gly	GGTC ACGA CGA Arg CCC Pro	TCGC GAC Asp GGC Gly CCG	GGG A TAC Tyr GTC Val 270 GCG	AGCAC GGC Gly 255 CCA Pro	GGGCGC AAG Lys CAC His	120 171
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248 249 250 250 250 250 260 260 260 260 260 261 267 267	3	(xi) ACGIC AGTCT AACTC CTG Leu GGT Gly GCC Ala	FEA (A	ATUREAL) NA B) LO QUENCE GGGGG GGGGC AGC Ser 260 CTG Leu	E: AME/K DEATI DE DE AGCCA CGGCG TCG TCG Ser CAC His	KEY: ON: ESCRI GG GG GG G GAA Glu CCC Pro	CDS 142. PTIC GCCAC GGCC AIG Met GAG Glu GCG Ala ATG Met	109 DN: S GGACC CCGAC Arg ATG Met CCT Pro 280	BEQ DEC TITE GEORGE ARG GGC Gly 265 TCT Ser	ID NO IGIGA GGGAC GCC Ala 250 AGC Ser GCA Ala	AACC BAGA AGC Ser GGC Gly CCG Pro	GGTC ACGA CGA Arg CCC Pro GCT Ala CTG Leu	GAC Asp GGC Gly CCG Pro 285 GGG	GGG A TAC Tyr GTC Val 270 GCG Ala	AGCAC GGC Gly 255 CCA Pro CCG Pro	GGGCGC AAG Lys CAC His CCA Pro	120 171 219 267
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248 249 250 250 250 250 260 -> 261 260 262 -> 265 271 276 -> 277 276	3	(xi) ACGIC AGTCT AACTC CTG Leu GGT Gly GCC Ala 290 CAG GIn	FEA (A (E) (A (E) (A (E) (E) (A (E)	ATUREAL) NAB) LOQUENO GGGGG GGGGG GGGGG GGGGG GGGGG GGGGG GGGG	E: AME/K AME	GEY: CON: ESCRI GC TO GG GI GC C GAA Glu CCC Pro TCC Ser AGC Ser 310 ATA	CDS 142. PTIC GCCAC GGCC AIG Met GAG Glu GCG Ala ATG Met 295 ATC Ile	109 DN: S GGACC CCGAC CCGC Arg ATG Met CCT Pro 280 ITC Phe GCT Ala GAA	GEQ IN GEO CEGG Arg GGC Gly 265 TCT Ser CTG Leu CTG Leu GAC	ID NOTIGITAL SECTION OF THE PROPERTY OF THE PR	ACC GAGA AGC Ser GGC Gly CCG Pro CTC Leu CTG Leu 315 ACT	GGTC ACGA CGA Arg CCC Pro GCT Ala CTG Leu 300 TAC Tyr	TCGC GAC Asp GGC Gly CCG Pro 285 GGG Gly TTT Phe	GGG A TAC TYT GTC Val 270 GCG Ala CTG Leu CGA Arg	AGCAC GGC Gly 255 CCA Pro CCG Pro GGA Gly GCG Ala	GGGCGC AAG Lys CAC His CCA Pro CTG Leu CAG Gln 320 AGA	120 171 219 267 315
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DATE: 03/12/2002 PATENT APPLICATION: US/09/873,829 TIME: 09:54:52

Input Set : N:\Crf3\RULE60\09873829.raw Output Set: N:\CRF3\03122002\1873829.raw

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	349	TGAT	TTCC	CTA C	GAATI	(GAAC	C AC	SATTO	GGAG	AGG	STATE	rccg	ATGO	TTAT	GA A	AAAA	CTTACA	1372
																	CTGAGA	1432

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,829

DATE: 03/12/2002 TIME 09 54:53

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set N:\CRF3\03122002\1873829.raw

1:31 M:220 C Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] £ 32 M:220 C Keyword misspelled or invalid format. [(B) FILING DATE:] I 261 M 336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.265 M:336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.269 M:336 W. Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 $\pm \cdot 273$ M.336 W. Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 1...277 M 336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3 L 281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:293 M:336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L-297 M.336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L-301 M.336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:317 M.336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:321 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID.3 L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:333 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3